

In the claims:

1. (Currently Amended) A composition comprising a purified Gux1 peptide, said Gux1 peptide comprising a glycoside hydrolase 48 (GH48) family catalytic domain ~~classified in family glycoside hydrolase 48 (GH48)~~ comprising residues 359-418 of SEQ ID NO. 5, a carbohydrate binding domain (CBD) type III, and a carbohydrate binding domain (CBD) type II.
2. (Original) The composition of claim 1 wherein the Gux1 peptide is further defined as comprising a linker and a signal peptide.
3. (Previously Presented) The composition of claim 1 wherein the GH48 catalytic domain of the Gux1 peptide is further defined as having a length of about 637 to about 643 amino acids.
4. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) type III of the Gux1 peptide is further defined as having a length of about 150 to about 156 amino acids.
5. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) type II of the Gux1 peptide is further defined as having a length of about 95 amino acids to about 105 amino acids in length.
6. (Currently Amended) A composition comprising a purified peptide, The composition of claim 3 said peptide comprising a catalytic domain classified in family glycoside hydrolase 48 (GH48) wherein the GH48 catalytic domain is further defined as having the sequence of SEQ ID NO: 5, a carbohydrate binding domain (CBD) type III, and a carbohydrate binding domain (CBD) type II.
7. (Currently Amended) The composition of claim [4] 6 wherein the carbohydrate binding domain (CBD) type III is further defined as having the sequence of SEQ ID NO: 4.

8. (Currently Amended) The composition of claim 6 wherein the carbohydrate binding domain (CBD) type II is further defined as having the sequence of SEQ ID NO:7.
9. (Previously Presented) The composition of claim 1 further defined as comprising, in combination, a sequence of SEQ ID NO: 4, SEQ ID NO: 5, and SEQ ID NO: 7.
10. (Currently Amended) An isolated ~~thermal tolerant Gux1~~ peptide having [a] the sequence of SEQ ID NO: 1.
11. (Currently Amended) The ~~Gux1~~ peptide of claim 10 further defined as ~~having an amino acid sequence~~ being encoded by a polynucleotide having the sequence of SEQ ID NO: 2.
- 12.-13. (Cancelled)
14. (Previously Presented) The composition of claim 1 wherein the Gux1 is further defined as comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5.
15. (Previously Presented) The composition of claim 1 wherein the Gux1 is further defined as comprising an amino acid sequence having at least 80% sequence identity to SEQ ID NO: 5.
16. (Previously Presented) The composition of claim 1 wherein the Gux1 is further defined as comprising an amino acid sequence having at least 70% sequence identity to SEQ ID NO: 5.

17. (Currently Amended) The composition of claim [1] 6 wherein the carbohydrate binding domain (CBD) type II Gux1 is further defined as comprising an amino acid sequence having at least ~~90%~~ 98% sequence identity to SEQ ID NO: 7.
18. (Currently Amended) The composition of claim [1] 6 wherein the carbohydrate binding domain (CBD) type III Gux1 is further defined as comprising an amino acid sequence having at least ~~90%~~ 98% sequence identity to SEQ ID NO: 4.
19. (Currently Amended) The composition of claim [1] 6 wherein the peptide Gux1 is further comprises a linker domain defined as comprising having an amino acid sequence having with at least ~~90%~~ 98% sequence identity to SEQ ID NO: 6.
20. (Currently Amended) The composition of claim [1] 6 wherein the peptide Gux1 is further defined as comprising an amino acid sequence having at least ~~90~~ 98% sequence identity to SEQ ID NO: 1.
21. (Currently Amended) The composition of claim [1] 6 wherein the peptide Gux1 is further defined as comprising an amino acid sequence encoded by a nucleic acid sequence that has at least 90% identity to the nucleic acid sequence of SEQ ID NO: 2.
22. (Cancelled)
23. (Currently Amended) The composition of claim ~~22~~ 6, wherein the peptide further comprises heterologous protein in frame with the Gux1 peptide of claim 1 is further ~~defined as a peptide tag~~.
24. (Previously Presented) The composition of claim 23 wherein the peptide tag is 6-His (SEQ ID NO: 8), thioredoxin, hemagglutinin, GST, or OmpA signal sequence tag.

25. (Currently Amended) The composition of claim 22 6 wherein the peptide further comprises heterologous protein is a substrate targeting moiety.

26-27. (Cancelled)

28. (Currently Amended) An isolated polypeptide molecule comprising:

- a) a sequence of SEQ ID NO: 4;
- b) a sequence of SEQ ID NO: 5;
- c) a sequence of SEQ ID NO: 6;
- d) a sequence of SEQ ID NO: 7;
- e) a sequence of SEQ ID NO: 1; or
- f) an amino acid sequence having at least 90% sequence identity with the amino acid sequence of a), b), c), d), or e);

29. (Currently Amended) The polypeptide molecule of claim 28, having at least 90 98% sequence identity with the amino acid sequence of a), b), c), d), or e).

30. (Previously Presented) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Previously Presented) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Previously Presented) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Presented) The fusion protein of claim 32, wherein the peptide tag is 6-His (SEQ ID NO: 8), thioredoxin, hemagglutinin, GST, or OmpA signal sequence tag.

34. (Previously Presented) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Previously Presented) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36-43 (Cancelled)

44. (Previously Presented) A composition comprising the polypeptide molecule of claim 29 and a carrier.

45. (Previously Presented) A composition comprising the polypeptide molecule of claim 30 and a carrier.

46-68 (Cancelled)

69. (Currently amended) The composition of claim [1] 6 further comprising a carrier.

70. (Currently Amended) The composition of claim [1] 6 wherein the ~~purified Gux-I~~ peptide is further defined as comprising a heterologous peptide or protein.

71. (Previously Presented) The composition of claim 70 wherein the heterologous peptide or protein comprises an immunoglobulin.

72. (Previously Presented) The composition of claim 70 wherein the heterologous peptide comprises a histidine tag.

73. (Previously Presented) The composition of claim 70 wherein the heterologous peptide comprises a leucine zipper.

74. (Previously Presented) The composition of claim 70 wherein the heterologous peptide comprises a fusion protein.
75. (Previously presented) A composition comprising a purified Gux1 peptide, said Gux1 peptide comprising a catalytic domain classified in family glycoside hydrolase 48 (GH48) having a sequence of SEQ ID NO. 5, a carbohydrate binding domain (CBD) type III, and a carbohydrate binding domain (CBD) type II
- 76 (Previously presented) The composition of claim 75 wherein the carbohydrate binding domain (CBD) type III is further defined as the sequence of SEQ ID NO: 4.
77. (Previously presented) The composition of claim 76 wherein the carbohydrate binding domain (CBD) type II is further defined as the sequence of SEQ ID NO:7.
78. (Currently amended) The composition of claim [1] 6 further defined as comprising, in combination, a sequence of SEQ ID NO: 4, SEQ ID NO: 5, and SEQ ID NO: 7 in that particular order.
79. (New) A purified polypeptide having a sequence with at least 95% identity to SEQ ID NO: 1.
80. (New) A purified polypeptide having a sequence with at least 98% identity to SEQ ID NO: 1.
81. (New) A composition comprising a purified polypeptide, said peptide comprising residues 359-418 of SEQ ID NO. 5.
82. (New) The composition of claim 81 wherein said polypeptide has ten or fewer conservative amino acid substitutions in SEQ ID NO. 5.

83. (New) The composition of claim 82 wherein said polypeptide has five or fewer conservative amino acid substitutions in SEQ ID NO. 5.

84. (New) The composition of claim 81 wherein said polypeptide has five or fewer conservative amino acid substitutions in residues 359-418 of SEQ ID NO. 5.